

H04714.txt
SEQUENZPROTOKOLL

<110> Henkel Kommanditgesellschaft auf Aktien

<120> Wasch- und Reinigungsmittel mit Hybrid-Alpha-Amylasen

<130> H 4714 PCT

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<150> DE 10138753.9-41

<151> 2001-08-07

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<170> PatentIn Ver. 2.1

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Thr	Arg	Glu	Ser	Gly	Tyr	Pro	Gln	Val	Phe	Tyr	Gly	Asp	Met	Tyr	Gly
		355					360					365			
Thr	Lys	Gly	Thr	Ser	Pro	Lys	Glu	Ile	Pro	Ser	Leu	Lys	Asp	Asn	Ile
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Glu	Pro	Ile	Leu	Lys	Ala	Arg	Lys	Glu	Tyr	Ala	Tyr	Gly	Pro	Gln	His
385					390					395					400
Asp	Tyr	Ile	Asp	His	Pro	Asp	Val	Ile	Gly	Trp	Thr	Arg	Glu	Gly	Asp
				405					410					415	
Ser	Ser	Ala	Ala	Lys	Ser	Gly	Leu	Ala	Ala	Leu	Ile	Thr	Asp	Gly	Pro
			420					425					430		
Gly	Gly	Ser	Lys	Arg	Met	Tyr	Ala	Gly	Leu	Lys	Asn	Ala	Gly	Glu	Thr
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Trp	Tyr	Asp	Ile	Thr	Gly	Asn	Arg	Ser	Asp	Thr	Val	Lys	Ile	Gly	Ser
	450					455					460				
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Val	Gln	Lys													

<210> 5
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 <212> DNA
 <213> Künstliche Sequenz

<220>
 <223> Beschreibung der künstlichen Sequenz:Fusion der
 Alpha-Amylase-Gene von B. licheniformis und B.
 amyloliquefaciens (AL34).

<220>
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 <222> (1)..(1446)

<400> 5

H04714.txt

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ggc	cag	cat	tgg	aaa	cga	ttg	cag	aat	gat	gcg	gaa	cat	tta	tcg	gat	96
Gly	Gln	His	Trp	Lys	Arg	Leu	Gln	Asn	Asp	Ala	Glu	His	Leu	Ser	Asp	
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Ile	Gly	Ile	Thr	Ala	Val	Trp	Ile	Pro	Pro	Ala	Tyr	Lys	Gly	Thr	Ser	
		35					40					45				
caa	gcg	gat	gtg	ggc	tac	ggt	gct	tac	gac	ctt	tat	gat	tta	ggg	gag	192
Gln	Ala	Asp	Val	Gly	Tyr	Gly	Ala	Tyr	Asp	Leu	Tyr	Asp	Leu	Gly	Glu	
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Phe	His	Gln	Lys	Gly	Thr	Val	Arg	Thr	Lys	Tyr	Gly	Thr	Lys	Gly	Glu	
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Leu	Gln	Ser	Ala	Ile	Lys	Ser	Leu	His	Ser	Arg	Asp	Ile	Asn	Val	Tyr	
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Gly	Asp	Val	Val	Ile	Asn	His	Lys	Gly	Gly	Ala	Asp	Ala	Thr	Glu	Asp	
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Val	Thr	Ala	Val	Glu	Val	Asp	Pro	Ala	Asp	Arg	Asn	Arg	Val	Ile	Ser	
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Gly	Glu	His	Arg	Ile	Lys	Ala	Trp	Thr	His	Phe	His	Phe	Pro	Gly	Arg	
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Gly	Ser	Thr	Tyr	Ser	Asp	Phe	Lys	Trp	His	Trp	Tyr	His	Phe	Asp	Gly	
145					150					155					160	
acc	gat	tgg	gac	gag	tcc	cga	aag	ctg	aac	cgc	atc	tat	aag	ttt	caa	528
Thr	Asp	Trp	Asp	Glu	Ser	Arg	Lys	Leu	Asn	Arg	Ile	Tyr	Lys	Phe	Gln	
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gga	aag	gct	tgg	gat	tgg	gaa	gtt	tcc	aat	gaa	aac	ggc	aac	tat	gat	576
Gly	Lys	Ala	Trp	Asp	Trp	Glu	Val	Ser	Asn	Glu	Asn	Gly	Asn	Tyr	Asp	
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tat	ttg	atg	tat	gcc	gac	atc	gat	tat	gac	cat	cct	gat	gtc	gca	gca	624
Tyr	Leu	Met	Tyr	Ala	Asp	Ile	Asp	Tyr	Asp	His	Pro	Asp	Val	Ala	Ala	
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gaa	att	aag	aga	tgg	ggc	act	tgg	tat	gcc	aat	gaa	ctg	caa	ttg	gac	672
Glu	Ile	Lys	Arg	Trp	Gly	Thr	Trp	Tyr	Ala	Asn	Glu	Leu	Gln	Leu	Asp	
	210					215					220					
ggt	ttc	cgt	ctt	gat	gct	gtc	aaa	cac	att	aaa	ttt	tct	ttt	ttg	cgg	720
Gly	Phe	Arg	Leu	Asp	Ala	Val	Lys	His	Ile	Lys	Phe	Ser	Phe	Leu	Arg	
225					230					235					240	
gat	tgg	gtt	aat	cat	gtc	agg	gaa	aaa	acg	ggg	aag	gaa	atg	ttt	acg	768
Asp	Trp	Val	Asn	His	Val	Arg	Glu	Lys	Thr	Gly	Lys	Glu	Met	Phe	Thr	
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Val	Ala	Glu	Tyr	Trp	Gln	Asn	Asp	Leu	Gly	Ala	Leu	Glu	Asn	Tyr	Leu	
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aac	aaa	aca	aat	ttt	aat	cat	tca	gtg	ttt	gac	gtg	ccg	ctt	cat	tat	864
Asn	Lys	Thr	Asn	Phe	Asn	His	Ser	Val	Phe	Asp	Val	Pro	Leu	His	Tyr	
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cag	ttc	cat	gct	gca	tcg	aca	cag	gga	ggc	ggc	tat	gat	atg	agg	aaa	912
Gln	Phe	His	Ala	Ala	Ser	Thr	Gln	Gly	Gly	Gly	Tyr	Asp	Met	Arg	Lys	
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ttg	ctg	aac	agt	acg	gtc	gtt	tcc	aag	cat	ccg	ttg	aaa	gcg	gtt	aca	960
Leu	Leu	Asn	Ser	Thr	Val	Val	Ser	Lys	His	Pro	Leu	Lys	Ala	Val	Thr	
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Phe	Val	Asp	Asn	His	Asp	Thr	Gln	Pro	Gly	Gln	Ser	Leu	Glu	Ser	Thr	
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Val	Gln	Thr	Trp	Phe	Lys	Pro	Leu	Ala	Tyr	Ala	Phe	Ile	Leu	Thr	Arg	
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Glu	Ser	Gly	Tyr	Pro	Gln	Val	Phe	Tyr	Gly	Asp	Met	Tyr	Gly	Thr	Lys	
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Gly	Asp	Ser	Gln	Arg	Glu	Ile	Pro	Ala	Leu	Lys	His	Lys	Ile	Glu	Pro	
		370				375					380					
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Ile	Leu	Lys	Ala	Arg	Lys	Gln	Tyr	Ala	Tyr	Gly	Ala	Gln	His	Asp	Tyr	
385					390					395					400	
ttc	gac	cac	cat	gac	att	gtc	ggc	tgg	aca	agg	gaa	ggc	gac	agc	tcg	1248
Phe	Asp	His	His	Asp	Ile	Val	Gly	Trp	Thr	Arg	Glu	Gly	Asp	Ser	Ser	
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gtt	gca	aat	tca	ggt	ttg	gcg	gca	tta	ata	aca	gac	gga	ccc	ggt	ggg	1296
Val	Ala	Asn	Ser	Gly	Leu	Ala	Ala	Leu	Ile	Thr	Asp	Gly	Pro	Gly	Gly	
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gca	aag	cga	atg	tat	gtc	ggc	cgg	caa	aac	gcc	ggt	gag	aca	tgg	cat	1344
Ala	Lys	Arg	Met	Tyr	Val	Gly	Arg	Gln	Asn	Ala	Gly	Glu	Thr	Trp	His	
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gac	att	acc	gga	aac	cgt	tcg	gag	ccg	gtt	gtc	atc	aat	tcg	gaa	ggc	1392
Asp	Ile	Thr	Gly	Asn	Arg	Ser	Glu	Pro	Val	Val	Ile	Asn	Ser	Glu	Gly	
	450					455					460					
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Trp	Gly	Glu	Phe	His	Val	Asn	Gly	Gly	Ser	Val	Ser	Ile	Tyr	Val	Gln	
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Arg																

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<212> PRT

<213> Künstliche Sequenz

<223> Beschreibung der künstlichen Sequenz:Fusion der
Alpha-Amylase-Gene von B. licheniformis und B.
amyloliquefaciens (AL34).

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Ile Gly Ile Thr Ala Val Trp Ile Pro Pro Ala Tyr Lys Gly Thr Ser
 35      40      45
Gln Ala Asp Val Gly Tyr Gly Ala Tyr Asp Leu Tyr Asp Leu Gly Glu
 50      55      60
Phe His Gln Lys Gly Thr Val Arg Thr Lys Tyr Gly Thr Lys Gly Glu
 65      70      75      80
Leu Gln Ser Ala Ile Lys Ser Leu His Ser Arg Asp Ile Asn Val Tyr
 85      90      95
Gly Asp Val Val Ile Asn His Lys Gly Gly Ala Asp Ala Thr Glu Asp
100      105      110
Val Thr Ala Val Glu Val Asp Pro Ala Asp Arg Asn Arg Val Ile Ser
115      120      125
Gly Glu His Arg Ile Lys Ala Trp Thr His Phe His Phe Pro Gly Arg
130      135      140
Gly Ser Thr Tyr Ser Asp Phe Lys Trp His Trp Tyr His Phe Asp Gly
145      150      155      160
Thr Asp Trp Asp Glu Ser Arg Lys Leu Asn Arg Ile Tyr Lys Phe Gln
165      170      175
Gly Lys Ala Trp Asp Trp Glu Val Ser Asn Glu Asn Gly Asn Tyr Asp
180      185      190
Tyr Leu Met Tyr Ala Asp Ile Asp Tyr Asp His Pro Asp Val Ala Ala
195      200      205
Glu Ile Lys Arg Trp Gly Thr Trp Tyr Ala Asn Glu Leu Gln Leu Asp
210      215      220
Gly Phe Arg Leu Asp Ala Val Lys His Ile Lys Phe Ser Phe Leu Arg
225      230      235      240
Asp Trp Val Asn His Val Arg Glu Lys Thr Gly Lys Glu Met Phe Thr
245      250      255
Val Ala Glu Tyr Trp Gln Asn Asp Leu Gly Ala Leu Glu Asn Tyr Leu
260      265      270
Asn Lys Thr Asn Phe Asn His Ser Val Phe Asp Val Pro Leu His Tyr
275      280      285
Gln Phe His Ala Ala Ser Thr Gln Gly Gly Gly Tyr Asp Met Arg Lys
290      295      300
Leu Leu Asn Ser Thr Val Val Ser Lys His Pro Leu Lys Ala Val Thr
305      310      315
Phe Val Asp Asn His Asp Thr Gln Pro Gly Gln Ser Leu Glu Ser Thr
320      325      330
Val Gln Thr Trp Phe Lys Pro Leu Ala Tyr Ala Phe Ile Leu Thr Arg
335      340      345
Glu Ser Gly Tyr Pro Gln Val Phe Tyr Gly Asp Met Tyr Gly Thr Lys
350      355      360
Gly Asp Ser Gln Arg Glu Ile Pro Ala Leu Lys His Lys Ile Glu Pro
365      370      375
Ile Leu Lys Ala Arg Lys Gln Tyr Ala Tyr Gly Ala Gln His Asp Tyr
380      385      390
Phe Asp His His Asp Ile Val Gly Trp Thr Arg Glu Gly Asp Ser Ser
395      400      405
Val Ala Asn Ser Gly Leu Ala Ala Leu Ile Thr Asp Gly Pro Gly Gly
410      415      420
Ala Lys Arg Met Tyr Val Gly Arg Gln Asn Ala Gly Glu Thr Trp His
425      430      435
440      445

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H04714.txt

Asp	Ile	Thr	Gly	Asn	Arg	Ser	Glu	Pro	Val	Val	Ile	Asn	Ser	Glu	Gly
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Trp	Gly	Glu	Phe	His	Val	Asn	Gly	Gly	Ser	Val	Ser	Ile	Tyr	Val	Gln
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Arg															

<210> 7
 <211> 1446
 <212> DNA
 <213> Künstliche Sequenz

<220>
 <223> Beschreibung der künstlichen Sequenz:Fusion der
 Alpha-Amylase-Gene von B. licheniformis und B.
 amyloliquefaciens (AL76).

<220>
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1				5					10					15			
ggc	cag	cat	tgg	aaa	cga	ttg	cag	aat	gat	gcg	gaa	cat	tta	tcg	gat		96
Gly	Gln	His	Trp	Lys	Arg	Leu	Gln	Asn	Asp	Ala	Glu	His	Leu	Ser	Asp		
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atc	gga	atc	act	gcc	gtc	tgg	att	cct	ccc	gca	tac	aaa	gga	ttg	agc		144
Ile	Gly	Ile	Thr	Ala	Val	Trp	Ile	Pro	Pro	Ala	Tyr	Lys	Gly	Leu	Ser		
		35				40						45					
caa	tcc	gat	aac	gga	tac	gga	cct	tat	gat	ttg	tat	gat	tta	gga	gaa		192
Gln	Ser	Asp	Asn	Gly	Tyr	Gly	Pro	Tyr	Asp	Leu	Tyr	Asp	Leu	Gly	Glu		
	50					55				60							
ttc	cag	caa	aaa	ggg	acg	gtc	aga	acg	aaa	tac	ggc	aca	aaa	gga	gag		240
Phe	Gln	Gln	Lys	Gly	Thr	Val	Arg	Thr	Lys	Tyr	Gly	Thr	Lys	Gly	Glu		
65				70					75					80			
ctg	caa	tct	gcg	atc	aaa	agt	ctt	cat	tcc	cgc	gac	att	aac	gtt	tac		288
Leu	Gln	Ser	Ala	Ile	Lys	Ser	Leu	His	Ser	Arg	Asp	Ile	Asn	Val	Tyr		
				85					90					95			
ggg	gat	gtg	gtc	atc	aac	cac	aaa	ggc	ggc	gct	gat	gcg	acc	gaa	gat		336
Gly	Asp	Val	Val	Ile	Asn	His	Lys	Gly	Gly	Ala	Asp	Ala	Thr	Glu	Asp		
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gta	acc	gcg	gtt	gaa	gtc	gat	ccc	gct	gac	cgc	aac	cgc	gta	att	tca		384
Val	Thr	Ala	Val	Glu	Val	Asp	Pro	Ala	Asp	Arg	Asn	Arg	Val	Ile	Ser		
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gga	gaa	cac	cga	att	aaa	gcc	tgg	aca	cat	ttt	cat	ttt	ccg	ggg	cgc		432
Gly	Glu	His	Arg	Ile	Lys	Ala	Trp	Thr	His	Phe	His	Phe	Pro	Gly	Arg		
	130					135					140						
ggc	agc	aca	tac	agc	gat	ttt	aaa	tgg	cat	tgg	tac	cat	ttt	gac	gga		480
Gly	Ser	Thr	Tyr	Ser	Asp	Phe	Lys	Trp	His	Trp	Tyr	His	Phe	Asp	Gly		
145					150					155					160		

H04714.txt

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Thr Asp Trp Asp Glu Ser Arg Lys Leu Asn Arg Ile Tyr Lys Phe Gln	
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	170
	175
gga aag gct tgg gat tgg gaa gtt tcc aat gaa aac ggc aac tat gat	576
Gly Lys Ala Trp Asp Trp Glu Val Ser Asn Glu Asn Gly Asn Tyr Asp	
	180
	185
	190
tat ttg atg tat gcc gac atc gat tat gac cat cct gat gtc gca gca	624
Tyr Leu Met Tyr Ala Asp Ile Asp Tyr Asp His Pro Asp Val Ala Ala	
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	200
	205
gaa att aag aga tgg ggc act tgg tat gcc aat gaa ctg caa ttg gac	672
Glu Ile Lys Arg Trp Gly Thr Trp Tyr Ala Asn Glu Leu Gln Leu Asp	
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	215
	220
ggt ttc cgt ctt gat gct gtc aaa cac att aaa ttt tct ttt ttg cgg	720
Gly Phe Arg Leu Asp Ala Val Lys His Ile Lys Phe Ser Phe Leu Arg	
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	235
gat tgg gtt aat cat gtc agg gaa aaa acg ggg aag gaa atg ttt acg	768
Asp Trp Val Asn His Val Arg Glu Lys Thr Gly Lys Glu Met Phe Thr	
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	250
	255
gta gct gaa tat tgg cag aat gac ttg ggc gcg ctg gaa aac tat ttg	816
Val Ala Glu Tyr Trp Gln Asn Asp Leu Gly Ala Leu Glu Asn Tyr Leu	
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aac aaa aca aat ttt aat cat tca gtg ttt gac gtg ccg ctt cat tat	864
Asn Lys Thr Asn Phe Asn His Ser Val Phe Asp Val Pro Leu His Tyr	
	275
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	285
cag ttc cat gct gca tcg aca cag gga ggc ggc tat gat atg agg aaa	912
Gln Phe His Ala Ala Ser Thr Gln Gly Gly Gly Tyr Asp Met Arg Lys	
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	295
	300
ttg ctg aac agt acg gtc gtt tcc aag cat ccg ttg aaa gcg gtt aca	960
Leu Leu Asn Ser Thr Val Val Ser Lys His Pro Leu Lys Ala Val Thr	
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Phe Val Asp Asn His Asp Thr Gln Pro Gly Gln Ser Leu Glu Ser Thr	
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gtc caa aca tgg ttt aag ccg ctt gct tac gct ttt att ctc aca agg	1056
Val Gln Thr Trp Phe Lys Pro Leu Ala Tyr Ala Phe Ile Leu Thr Arg	
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Glu Ser Gly Tyr Pro Gln Val Phe Tyr Gly Asp Met Tyr Gly Thr Lys	
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gga gac tcc cag cgc gaa att cct gcc ttg aaa cac aaa att gaa ccg	1152
Gly Asp Ser Gln Arg Glu Ile Pro Ala Leu Lys His Lys Ile Glu Pro	
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	375
	380
atc tta aaa gcg aga aaa cag tat gcg tac gga gca cag cat gat tat	1200
Ile Leu Lys Ala Arg Lys Gln Tyr Ala Tyr Gly Ala Gln His Asp Tyr	
	385
	390
	395
ttc gac cac cat gac att gtc ggc tgg aca agg gaa ggc gac agc tcg	1248
Phe Asp His His Asp Ile Val Gly Trp Thr Arg Glu Gly Asp Ser Ser	
	405
	410
	415

H04714.txt

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Val Ala Asn Ser Gly Leu Ala Ala Leu Ile Thr Asp Gly Pro Gly Gly	
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gca aag cga atg tat gtc ggc cgg caa aac gcc ggt gag aca tgg cat	1344
Ala Lys Arg Met Tyr Val Gly Arg Gln Asn Ala Gly Glu Thr Trp His	
	435 440 445
gac att acc gga aac cgt tgc gag ccg gtt gtc atc aat tcg gaa ggc	1392
Asp Ile Thr Gly Asn Arg Ser Glu Pro Val Val Ile Asn Ser Glu Gly	
	450 455 460
tgg gga gag ttt cac gta aac ggc ggg tcg gtt tca att tat gtt caa	1440
Trp Gly Glu Phe His Val Asn Gly Gly Ser Val Ser Ile Tyr Val Gln	
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aga tag	1446
Arg	

<210> 8
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 <213> Künstliche Sequenz
 <223> Beschreibung der künstlichen Sequenz:Fusion der
 Alpha-Amylase-Gene von B. licheniformis und B.
 amyloliquefaciens (AL76).

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Ile Gly Ile Thr Ala Val Trp Ile Pro Pro Ala Tyr Lys Gly Leu Ser	
35 40 45	
Gln Ser Asp Asn Gly Tyr Gly Pro Tyr Asp Leu Tyr Asp Leu Gly Glu	
50 55 60	
Phe Gln Gln Lys Gly Thr Val Arg Thr Lys Tyr Gly Thr Lys Gly Glu	
65 70 75 80	
Leu Gln Ser Ala Ile Lys Ser Leu His Ser Arg Asp Ile Asn Val Tyr	
85 90 95	
Gly Asp Val Val Ile Asn His Lys Gly Gly Ala Asp Ala Thr Glu Asp	
100 105 110	
Val Thr Ala Val Glu Val Asp Pro Ala Asp Arg Asn Arg Val Ile Ser	
115 120 125	
Gly Glu His Arg Ile Lys Ala Trp Thr His Phe His Phe Pro Gly Arg	
130 135 140	
Gly Ser Thr Tyr Ser Asp Phe Lys Trp His Trp Tyr His Phe Asp Gly	
145 150 155 160	
Thr Asp Trp Asp Glu Ser Arg Lys Leu Asn Arg Ile Tyr Lys Phe Gln	
165 170 175	
Gly Lys Ala Trp Asp Trp Glu Val Ser Asn Glu Asn Gly Asn Tyr Asp	
180 185 190	
Tyr Leu Met Tyr Ala Asp Ile Asp Tyr Asp His Pro Asp Val Ala Ala	
195 200 205	
Glu Ile Lys Arg Trp Gly Thr Trp Tyr Ala Asn Glu Leu Gln Leu Asp	
210 215 220	
Gly Phe Arg Leu Asp Ala Val Lys His Ile Lys Phe Ser Phe Leu Arg	
225 230 235 240	
Asp Trp Val Asn His Val Arg Glu Lys Thr Gly Lys Glu Met Phe Thr	
245 250 255	
Val Ala Glu Tyr Trp Gln Asn Asp Leu Gly Ala Leu Glu Asn Tyr Leu	

H04714.txt

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Gln Phe His Ala Ala Ser Thr Gln Gly Gly Gly Tyr Asp Met Arg Lys
      290      295      300
Leu Leu Asn Ser Thr Val Val Ser Lys His Pro Leu Lys Ala Val Thr
      305      310      315
Phe Val Asp Asn His Asp Thr Gln Pro Gly Gln Ser Leu Glu Ser Thr
      325      330      335
Val Gln Thr Trp Phe Lys Pro Leu Ala Tyr Ala Phe Ile Leu Thr Arg
      340      345      350
Glu Ser Gly Tyr Pro Gln Val Phe Tyr Gly Asp Met Tyr Gly Thr Lys
      355      360      365
Gly Asp Ser Gln Arg Glu Ile Pro Ala Leu Lys His Lys Ile Glu Pro
      370      375      380
Ile Leu Lys Ala Arg Lys Gln Tyr Ala Tyr Gly Ala Gln His Asp Tyr
      385      390      395
Phe Asp His His Asp Ile Val Gly Trp Thr Arg Glu Gly Asp Ser Ser
      405      410      415
Val Ala Asn Ser Gly Leu Ala Ala Leu Ile Thr Asp Gly Pro Gly Gly
      420      425      430
Ala Lys Arg Met Tyr Val Gly Arg Gln Asn Ala Gly Glu Thr Trp His
      435      440      445
Asp Ile Thr Gly Asn Arg Ser Glu Pro Val Val Ile Asn Ser Glu Gly
      450      455      460
Trp Gly Glu Phe His Val Asn Gly Gly Ser Val Ser Ile Tyr Val Gln
      465      470      475
Arg

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<210> 9

<211> 1446

<212> DNA

<213> Künstliche Sequenz

<220>

<223> Beschreibung der künstlichen Sequenz: Fusion der
Alpha-Amylase-Gene von *B. licheniformis* und *B.*
amyloliquefaciens (AL112).

<220>

<221> CDS

<222> (1)..(1446)

<400> 9

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gta aat ggc acg ctg atg cag tat ttt gaa tgg tat acg ccg aac gac   48
Val Asn Gly Thr Leu Met Gln Tyr Phe Glu Trp Tyr Thr Pro Asn Asp
  1          5          10          15

ggc cag cat tgg aaa cga ttg cag aat gat gcg gaa cat tta tcg gat   96
Gly Gln His Trp Lys Arg Leu Gln Asn Asp Ala Glu His Leu Ser Asp
          20          25          30

atc gga atc act gcc gtc tgg att cct ccc gca tac aaa gga ttg agc   144
Ile Gly Ile Thr Ala Val Trp Ile Pro Pro Ala Tyr Lys Gly Leu Ser
          35          40          45

caa tcc gat aac gga tac gga cct tat gat ttg tat gat tta gga gaa   192
Gln Ser Asp Asn Gly Tyr Gly Pro Tyr Asp Leu Tyr Asp Leu Gly Glu
          50          55          60

ttc cag caa aaa ggg acg gtc aga acg aaa tac ggc aca aaa tca gag   240

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H04714.txt

Phe 65	Gln	Gln	Lys	Gly	Thr 70	Val	Arg	Thr	Lys	Tyr 75	Gly	Thr	Lys	Ser	Glu 80	
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gga Gly	gat Asp	gtg Val	gtt Val 100	ttg Leu	aat Asn	cat His	aag Lys	gct Ala 105	ggt Gly	gct Ala	gat Asp	gca Ala	aca Thr 110	gaa Glu	gat Asp	336
gta Val	acc Thr	gcg Ala 115	gtt Val	gaa Glu	gtc Val	gat Asp	ccc Pro 120	gct Ala	gac Asp	cgc Arg	aac Asn	cgc Arg 125	gta Val	att Ile	tca Ser	384
gga Gly	gaa Glu 130	cac His	cga Arg	att Ile	aaa Lys	gcc Ala 135	tgg Trp	aca Thr	cat His	ttt Phe	cat His 140	ttt Phe	ccg Pro	ggg Gly	cgc Arg	432
ggc Gly 145	agc Ser	aca Thr	tac Tyr	agc Ser	gat Asp 150	ttt Phe	aaa Lys	tgg Trp	cat His	tgg Trp 155	tac Tyr	cat His	ttt Phe	gac Asp	gga Gly 160	480
acc Thr	gat Asp	tgg Trp	gac Asp	gag Glu 165	tcc Ser	cga Arg	aag Lys	ctg Leu	aac Asn 170	cgc Arg	atc Ile	tat Tyr	aag Lys	ttt Phe 175	caa Gln	528
gga Gly	aag Lys	gct Ala	tgg Trp 180	gat Asp	tgg Trp	gaa Glu	gtt Val	tcc Ser 185	aat Asn	gaa Glu	aac Asn	ggc Gly 190	aac Asn	tat Tyr	gat Asp	576
tat Tyr	ttg Leu	atg Met 195	tat Tyr	gcc Ala	gac Asp	atc Ile	gat Asp 200	tat Tyr	gac Asp	cat His	cct Pro	gat Asp 205	gtc Val	gca Ala	gca Ala	624
gaa Glu	att Ile 210	aag Lys	aga Arg	tgg Trp	ggc Gly	act Thr 215	tgg Trp	tat Tyr	gcc Ala	aat Asn	gaa Glu 220	ctg Leu	caa Gln	ttg Leu	gac Asp	672
ggt Gly 225	ttc Phe	cgt Arg	ctt Leu	gat Asp	gct Ala 230	gtc Val	aaa Lys	cac His	att Ile	aaa Lys 235	ttt Phe	tct Ser	ttt Phe	ttg Leu	cgg Arg 240	720
gat Asp	tgg Trp	gtt Val	aat Asn	cat His 245	gtc Val	agg Arg	gaa Glu	aaa Lys	acg Thr 250	ggg Gly	aag Lys	gaa Glu	atg Met	ttt Phe 255	acg Thr	768
gta Val	gct Ala	gaa Glu	tat Tyr 260	tgg Trp	cag Gln	aat Asn	gac Asp	ttg Leu 265	ggc Gly	gcg Ala	ctg Leu	gaa Glu	aac Asn 270	tat Tyr	ttg Leu	816
aac Asn	aaa Lys	aca Thr 275	aat Asn	ttt Phe	aat Asn	cat His	tca Ser 280	gtg Val	ttt Phe	gac Asp	gtg Val	ccg Pro 285	ctt Leu	cat His	tat Tyr	864
cag Gln	ttc Phe 290	cat His	gct Ala	gca Ala	tcg Ser	aca Thr 295	cag Gln	gga Gly	ggc Gly	ggc Gly	tat Tyr 300	gat Asp	atg Met	agg Arg	aaa Lys	912
ttg Leu 305	ctg Leu	aac Asn	agt Ser	acg Thr	gtc Val 310	gtt Val	tcc Ser	aag Lys	cat His	ccg Pro 315	ttg Leu	aaa Lys	gcg Ala	gtt Val	aca Thr 320	960

H04714.txt

ttt gtc gat aac cat gat aca cag ccg ggg caa tcg ctt gag tcg act	1008
Phe Val Asp Asn His 325 Asp Thr Gln Pro Gly 330 Gln Ser Leu Glu Ser 335 Thr	
gtc caa aca tgg ttt aag ccg ctt gct tac gct ttt att ctc aca agg	1056
Val Gln Thr Trp 340 Phe Lys Pro Leu Ala 345 Tyr Ala Phe Ile Leu 350 Thr Arg	
gaa tct gga tac cct cag gtt ttc tac ggg gat atg tac ggg acg aaa	1104
Glu Ser Gly 355 Tyr Pro Gln Val Phe 360 Tyr Gly Asp Met Tyr 365 Gly Thr Lys	
gga gac tcc cag cgc gaa att cct gcc ttg aaa cac aaa att gaa ccg	1152
Gly Asp 370 Ser Gln Arg Glu 375 Ile Pro Ala Leu Lys 380 His Lys Ile Glu Pro	
atc tta aaa gcg aga aaa cag tat gcg tac gga gca cag cat gat tat	1200
Ile Leu Lys Ala Arg 390 Gln Tyr Ala Tyr Gly 395 Ala Gln His Asp Tyr 400	
ttc gac cac cat gac att gtc ggc tgg aca agg gaa ggc gac agc tcg	1248
Phe Asp His His Asp 405 Ile Val Gly Trp 410 Thr Arg Glu Gly Asp 415 Ser Ser	
gtt gca aat tca ggt ttg gcg gca tta ata aca gac gga ccc ggt ggg	1296
Val Ala Asn Ser 420 Gly Leu Ala Ala Leu 425 Ile Thr Asp Gly Pro 430 Gly Gly	
gca aag cga atg tat gtc ggc cgg caa aac gcc ggt gag aca tgg cat	1344
Ala Lys Arg Met Tyr Val Gly Arg 440 Gln Asn Ala Gly 445 Glu Thr Trp His	
gac att acc gga aac cgt tcg gag ccg gtt gtc atc aat tcg gaa ggc	1392
Asp Ile Thr Gly Asn Arg Ser 455 Glu Pro Val Val Ile 460 Asn Ser Glu Gly	
tgg gga gag ttt cac gta aac ggc ggg tcg gtt tca att tat gtt caa	1440
Trp Gly Glu Phe His 470 Val Asn Gly Gly Ser Val 475 Ser Ile Tyr Val Gln 480	
aga tag	1446
Arg	

<210> 10

<211> 481

<212> PRT

<213> Künstliche Sequenz

<223> Beschreibung der künstlichen Sequenz: Fusion der
Alpha-Amylase-Gene von B. licheniformis und B.
amyloliquefaciens (AL112).

<400> 10

Val	Asn	Gly	Thr	Leu	Met	Gln	Tyr	Phe	Glu	Trp	Tyr	Thr	Pro	Asn	Asp
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Gly	Gln	His	Trp	Lys	Arg	Leu	Gln	Asn	Asp	Ala	Glu	His	Leu	Ser	Asp
			20					25					30		
Ile	Gly	Ile	Thr	Ala	Val	Trp	Ile	Pro	Pro	Ala	Tyr	Lys	Gly	Leu	Ser
		35					40					45			
Gln	Ser	Asp	Asn	Gly	Tyr	Gly	Pro	Tyr	Asp	Leu	Tyr	Asp	Leu	Gly	Glu
	50					55					60				
Phe	Gln	Gln	Lys	Gly	Thr	Val	Arg	Thr	Lys	Tyr	Gly	Thr	Lys	Ser	Glu
65					70				75						80

H04714.txt

Leu	Gln	Asp	Ala	Ile	Gly	Ser	Leu	His	Ser	Arg	Asn	Val	Gln	Val	Tyr
				85					90					95	
Gly	Asp	Val	Val	Leu	Asn	His	Lys	Ala	Gly	Ala	Asp	Ala	Thr	Glu	Asp
			100					105					110		
Val	Thr	Ala	Val	Glu	Val	Asp	Pro	Ala	Asp	Arg	Asn	Arg	Val	Ile	Ser
		115					120					125			
Gly	Glu	His	Arg	Ile	Lys	Ala	Trp	Thr	His	Phe	His	Phe	Pro	Gly	Arg
	130					135					140				
Gly	Ser	Thr	Tyr	Ser	Asp	Phe	Lys	Trp	His	Trp	Tyr	His	Phe	Asp	Gly
145					150					155					160
Thr	Asp	Trp	Asp	Glu	Ser	Arg	Lys	Leu	Asn	Arg	Ile	Tyr	Lys	Phe	Gln
				165					170					175	
Gly	Lys	Ala	Trp	Asp	Trp	Glu	Val	Ser	Asn	Glu	Asn	Gly	Asn	Tyr	Asp
			180					185					190		
Tyr	Leu	Met	Tyr	Ala	Asp	Ile	Asp	Tyr	Asp	His	Pro	Asp	Val	Ala	Ala
		195					200					205			
Glu	Ile	Lys	Arg	Trp	Gly	Thr	Trp	Tyr	Ala	Asn	Glu	Leu	Gln	Leu	Asp
	210					215					220				
Gly	Phe	Arg	Leu	Asp	Ala	Val	Lys	His	Ile	Lys	Phe	Ser	Phe	Leu	Arg
225					230					235					240
Asp	Trp	Val	Asn	His	Val	Arg	Glu	Lys	Thr	Gly	Lys	Glu	Met	Phe	Thr
				245					250					255	
Val	Ala	Glu	Tyr	Trp	Gln	Asn	Asp	Leu	Gly	Ala	Leu	Glu	Asn	Tyr	Leu
			260					265					270		
Asn	Lys	Thr	Asn	Phe	Asn	His	Ser	Val	Phe	Asp	Val	Pro	Leu	His	Tyr
		275					280					285			
Gln	Phe	His	Ala	Ala	Ser	Thr	Gln	Gly	Gly	Gly	Tyr	Asp	Met	Arg	Lys
	290					295					300				
Leu	Leu	Asn	Ser	Thr	Val	Val	Ser	Lys	His	Pro	Leu	Lys	Ala	Val	Thr
305					310					315					320
Phe	Val	Asp	Asn	His	Asp	Thr	Gln	Pro	Gly	Gln	Ser	Leu	Glu	Ser	Thr
				325					330					335	
Val	Gln	Thr	Trp	Phe	Lys	Pro	Leu	Ala	Tyr	Ala	Phe	Ile	Leu	Thr	Arg
			340					345					350		
Glu	Ser	Gly	Tyr	Pro	Gln	Val	Phe	Tyr	Gly	Asp	Met	Tyr	Gly	Thr	Lys
		355					360					365			
Gly	Asp	Ser	Gln	Arg	Glu	Ile	Pro	Ala	Leu	Lys	His	Lys	Ile	Glu	Pro
	370					375					380				
Ile	Leu	Lys	Ala	Arg	Lys	Gln	Tyr	Ala	Tyr	Gly	Ala	Gln	His	Asp	Tyr
385					390					395					400
Phe	Asp	His	His	Asp	Ile	Val	Gly	Trp	Thr	Arg	Glu	Gly	Asp	Ser	Ser
				405					410					415	
Val	Ala	Asn	Ser	Gly	Leu	Ala	Ala	Leu	Ile	Thr	Asp	Gly	Pro	Gly	Gly
			420					425					430		
Ala	Lys	Arg	Met	Tyr	Val	Gly	Arg	Gln	Asn	Ala	Gly	Glu	Thr	Trp	His
		435					440					445			
Asp	Ile	Thr	Gly	Asn	Arg	Ser	Glu	Pro	Val	Val	Ile	Asn	Ser	Glu	Gly
	450					455					460				
Trp	Gly	Glu	Phe	His	Val	Asn	Gly	Gly	Ser	Val	Ser	Ile	Tyr	Val	Gln
465					470					475					480
Arg															

<210> 11
 <211> 1452
 <212> DNA
 <213> Künstliche Sequenz

<220>
 <223> Beschreibung der künstlichen Sequenz: Fusion der
 Alpha-Amylase-Gene von B. licheniformis und B.
 amyloliquefaciens (AL256).

H04714.txt

<220>

<221> CDS

<222> (1)..(1452)

<400> 11

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ggc cag cat tgg aaa cga ttg cag aat gat gcg gaa cat tta tcg gat	96
Gly Gln His Trp Lys Arg Leu Gln Asn Asp Ala Glu His Leu Ser Asp	
20 25 30	
atc gga atc act gcc gtc tgg att cct ccc gca tac aaa gga ttg agc	144
Ile Gly Ile Thr Ala Val Trp Ile Pro Pro Ala Tyr Lys Gly Leu Ser	
35 40 45	
caa tcc gat aac gga tac gga cct tat gat ttg tat gat tta gga gaa	192
Gln Ser Asp Asn Gly Tyr Gly Pro Tyr Asp Leu Tyr Asp Leu Gly Glu	
50 55 60	
ttc cag caa aaa ggg acg gtc aga acg aaa tac ggc aca aaa tca gag	240
Phe Gln Gln Lys Gly Thr Val Arg Thr Lys Tyr Gly Thr Lys Ser Glu	
65 70 75 80	
ctt caa gat gcg atc ggc tca ctg cat tcc cgg aac gtc caa gta tac	288
Leu Gln Asp Ala Ile Gly Ser Leu His Ser Arg Asn Val Gln Val Tyr	
85 90 95	
gga gat gtg gtt ttg aat cat aag gct ggt gct gat gca aca gaa gat	336
Gly Asp Val Val Leu Asn His Lys Ala Gly Ala Asp Ala Thr Glu Asp	
100 105 110	
gta act gcc gtc gaa gtc aat ccg gcc aat aga aat cag gaa act tcg	384
Val Thr Ala Val Glu Val Asn Pro Ala Asn Arg Asn Gln Glu Thr Ser	
115 120 125	
gag gaa tat caa atc aaa gcg tgg acg gat ttt cgt ttt ccg ggc cgt	432
Glu Glu Tyr Gln Ile Lys Ala Trp Thr Asp Phe Arg Phe Pro Gly Arg	
130 135 140	
gga aac acg tac agt gat ttt aaa tgg cat tgg tat cat ttc gac gga	480
Gly Asn Thr Tyr Ser Asp Phe Lys Trp His Trp Tyr His Phe Asp Gly	
145 150 155 160	
gcg gac tgg gat gaa tcc cgg aag atc agc cgc atc ttt aag ttt cgt	528
Ala Asp Trp Asp Glu Ser Arg Lys Ile Ser Arg Ile Phe Lys Phe Arg	
165 170 175	
ggg gaa gga aaa gcg tgg gat tgg gaa gta tca agt gaa aac ggc aac	576
Gly Glu Gly Lys Ala Trp Asp Trp Glu Val Ser Ser Glu Asn Gly Asn	
180 185 190	
tat gac tat tta atg tat gct gat gtt gac tac gac cac cct gat gtc	624
Tyr Asp Tyr Leu Met Tyr Ala Asp Val Asp Tyr Asp His Pro Asp Val	
195 200 205	
gtg gca gag aca aaa aaa tgg ggt atc tgg tat gcg aat gaa ctg tca	672
Val Ala Glu Thr Lys Lys Trp Gly Ile Trp Tyr Ala Asn Glu Leu Ser	
210 215 220	
tta gac ggc ttc cgt att gat gcc gcc aaa cat att aaa ttt tca ttt	720

H04714.txt

Leu 225	Asp	Gly	Phe	Arg	Ile 230	Asp	Ala	Ala	Lys	His 235	Ile	Lys	Phe	Ser	Phe 240	
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tat Tyr	ttg Leu	aac Asn 275	aaa Lys	aca Thr	aat Asn	ttt Phe	aat Asn 280	cat His	tca Ser	gtg Val	ttt Phe	gac Asp 285	gtg Val	ccg Pro	ctt Leu	864
cat His	tat Tyr 290	cag Gln	ttc Phe	cat His	gct Ala	gca Ala 295	tcg Ser	aca Thr	cag Gln	gga Gly	ggc Gly 300	ggc Gly	tat Tyr	gat Asp	atg Met	912
agg Arg 305	aaa Lys	ttg Leu	ctg Leu	aac Asn	agt Ser 310	acg Thr	gtc Val	gtt Val	tcc Ser	aag Lys 315	cat His	ccg Pro	ttg Leu	aaa Lys	gcg Ala 320	960
gtt Val	aca Thr	ttt Phe	gtc Val	gat Asp 325	aac Asn	cat His	gat Asp	aca Thr	cag Gln 330	ccg Pro	ggg Gly	caa Gln	tcg Ser	ctt Leu 335	gag Glu	1008
tcg Ser	act Thr	gtc Val	caa Gln 340	aca Thr	tgg Trp	ttt Phe	aag Lys	ccg Pro 345	ctt Leu	gct Ala	tac Tyr	gct Ala	ttt Phe 350	att Ile	ctc Leu	1056
aca Thr	agg Arg	gaa Glu 355	tct Ser	gga Gly	tac Tyr	cct Pro	cag Gln 360	gtt Val	ttc Phe	tac Tyr	ggg Gly	gat Asp 365	atg Met	tac Tyr	ggg Gly	1104
acg Thr	aaa Lys 370	gga Gly	gac Asp	tcc Ser	cag Gln	cgc Arg 375	gaa Glu	att Ile	cct Pro	gcc Ala	ttg Leu 380	aaa Lys	cac His	aaa Lys	att Ile	1152
gaa Glu 385	ccg Pro	atc Ile	tta Leu	aaa Lys	gcg Ala 390	aga Arg	aaa Lys	cag Gln	tat Tyr	gcg Ala 395	tac Tyr	gga Gly	gca Ala	cag Gln	cat His 400	1200
gat Asp	tat Tyr	ttc Phe	gac Asp	cac His 405	cat His	gac Asp	att Ile	gtc Val	ggc Gly 410	tgg Trp	aca Thr	agg Arg	gaa Glu	ggc Gly 415	gac Asp	1248
agc Ser	tcg Ser	gtt Val	gca Ala 420	aat Asn	tca Ser	ggt Gly	ttg Leu 425	gcg Ala	gca Ala	tta Leu	ata Ile	aca Thr	gac Asp 430	gga Gly	ccc Pro	1296
ggt Gly	ggg Gly	gca Ala 435	aag Lys	cga Arg	atg Met	tat Tyr	gtc Val 440	ggc Gly	cgg Arg	caa Gln	aac Asn	gcc Ala 445	ggt Gly	gag Glu	aca Thr	1344
tgg Trp	cat His 450	gac Asp	att Ile	acc Thr	gga Gly	aac Asn 455	cgt Arg	tcg Ser	gag Glu	ccg Pro	gtt Val 460	gtc Val	atc Ile	aat Asn	tcg Ser	1392
gaa Glu 465	ggc Gly	tgg Trp	gga Gly	gag Glu	ttt Phe 470	cac His	gta Val	aac Asn	ggc Gly	ggg Gly 475	tcg Ser	gtt Val	tca Ser	att Ile	tat Tyr 480	1440

gtt caa aga tag
Val Gln Arg

<210> 12
<211> 483
<212> PRT
<213> Künstliche Sequenz
<223> Beschreibung der künstlichen Sequenz:Fusion der
Alpha-Amylase-Gene von B. licheniformis und B.
amyloliquefaciens (AL256).

<400> 12
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35 40 45
Gln Ser Asp Asn Gly Tyr Gly Pro Tyr Asp Leu Tyr Asp Leu Gly Glu
50 55 60
Phe Gln Gln Lys Gly Thr Val Arg Thr Lys Tyr Gly Thr Lys Ser Glu
65 70 75 80
Leu Gln Asp Ala Ile Gly Ser Leu His Ser Arg Asn Val Gln Val Tyr
85 90 95
Gly Asp Val Val Leu Asn His Lys Ala Gly Ala Asp Ala Thr Glu Asp
100 105 110
Val Thr Ala Val Glu Val Asn Pro Ala Asn Arg Asn Gln Glu Thr Ser
115 120 125
Glu Glu Tyr Gln Ile Lys Ala Trp Thr Asp Phe Arg Phe Pro Gly Arg
130 135 140
Gly Asn Thr Tyr Ser Asp Phe Lys Trp His Trp Tyr His Phe Asp Gly
145 150 155 160
Ala Asp Trp Asp Glu Ser Arg Lys Ile Ser Arg Ile Phe Lys Phe Arg
165 170 175
Gly Glu Gly Lys Ala Trp Asp Trp Glu Val Ser Ser Glu Asn Gly Asn
180 185 190
Tyr Asp Tyr Leu Met Tyr Ala Asp Val Asp Tyr Asp His Pro Asp Val
195 200 205
Val Ala Glu Thr Lys Lys Trp Gly Ile Trp Tyr Ala Asn Glu Leu Ser
210 215 220
Leu Asp Gly Phe Arg Ile Asp Ala Ala Lys His Ile Lys Phe Ser Phe
225 230 235 240
Leu Arg Asp Trp Val Gln Ala Val Arg Gln Ala Thr Gly Lys Glu Met
245 250 255
Phe Thr Val Ala Glu Tyr Trp Gln Asn Asp Leu Gly Ala Leu Glu Asn
260 265 270
Tyr Leu Asn Lys Thr Asn Phe Asn His Ser Val Phe Asp Val Pro Leu
275 280 285
His Tyr Gln Phe His Ala Ala Ser Thr Gln Gly Gly Tyr Asp Met
290 295 300
Arg Lys Leu Leu Asn Ser Thr Val Val Ser Lys His Pro Leu Lys Ala
305 310 315 320
Val Thr Phe Val Asp Asn His Asp Thr Gln Pro Gly Gln Ser Leu Glu
325 330 335
Ser Thr Val Gln Thr Trp Phe Lys Pro Leu Ala Tyr Ala Phe Ile Leu
340 345 350
Thr Arg Glu Ser Gly Tyr Pro Gln Val Phe Tyr Gly Asp Met Tyr Gly
355 360 365
Thr Lys Gly Asp Ser Gln Arg Glu Ile Pro Ala Leu Lys His Lys Ile
370 375 380
Glu Pro Ile Leu Lys Ala Arg Lys Gln Tyr Ala Tyr Gly Ala Gln His
385 390 395 400

H04714.txt

Asp	Tyr	Phe	Asp	His	His	Asp	Ile	Val	Gly	Trp	Thr	Arg	Glu	Gly	Asp
				405					410					415	
Ser	Ser	Val	Ala	Asn	Ser	Gly	Leu	Ala	Ala	Leu	Ile	Thr	Asp	Gly	Pro
			420					425					430		
Gly	Gly	Ala	Lys	Arg	Met	Tyr	Val	Gly	Arg	Gln	Asn	Ala	Gly	Glu	Thr
		435					440					445			
Trp	His	Asp	Ile	Thr	Gly	Asn	Arg	Ser	Glu	Pro	Val	Val	Ile	Asn	Ser
	450					455					460				
Glu	Gly	Trp	Gly	Glu	Phe	His	Val	Asn	Gly	Gly	Ser	Val	Ser	Ile	Tyr
465					470					475					480
Val	Gln	Arg													

<210> 13
 <211> 1452
 <212> DNA
 <213> Künstliche Sequenz

<220>
 <223> Beschreibung der künstlichen Sequenz: Fusion der
 Alpha-Amylase-Gene von B. licheniformis und B.
 amyloliquefaciens (ALA34-84).

<220>
 <221> CDS
 <222> (1)..(1452)

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1 5 10 15	
ggc cag cat tgg aaa cga ttg cag aat gat gcg gaa cat tta tcg gat	96
Gly Gln His Trp Lys Arg Leu Gln Asn Asp Ala Glu His Leu Ser Asp	
20 25 30	
atc ggt att act gcc gtc tgg att ccc ccg gca tat aag gga acg agc	144
Ile Gly Ile Thr Ala Val Trp Ile Pro Pro Ala Tyr Lys Gly Thr Ser	
35 40 45	
caa gcg gat gtg ggc tac ggt gct tac gac ctt tat gat tta ggg gag	192
Gln Ala Asp Val Gly Tyr Gly Ala Tyr Asp Leu Tyr Asp Leu Gly Glu	
50 55 60	
ttt cat caa aaa ggg acg gtt cgg aca aag tac ggc aca aaa gga gag	240
Phe His Gln Lys Gly Thr Val Arg Thr Lys Tyr Gly Thr Lys Gly Glu	
65 70 75 80	
ctg caa tct gcg atc ggc tca ctg cat tcc cgg aac gtc caa gta tac	288
Leu Gln Ser Ala Ile Gly Ser Leu His Ser Arg Asn Val Gln Val Tyr	
85 90 95	
gga gat gtg gtt ttg aat cat aag gct ggt gct gat gca aca gaa gat	336
Gly Asp Val Val Leu Asn His Lys Ala Gly Ala Asp Ala Thr Glu Asp	
100 105 110	
gta act gcc gtc gaa gtc aat ccg gcc aat aga aat cag gaa act tcg	384
Val Thr Ala Val Glu Val Asn Pro Ala Asn Arg Asn Gln Glu Thr Ser	
115 120 125	
gag gaa tat caa atc aaa gcg tgg acg gat ttt cgt ttt ccg ggc cgt	432
Glu Glu Tyr Gln Ile Lys Ala Trp Thr Asp Phe Arg Phe Pro Gly Arg	

H04714.txt
140

130	135																
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gcg Ala	gac Asp	tgg Trp	gat Asp	gaa Glu 165	tcc Ser	cgg Arg	aag Lys	atc Ile	agc Ser 170	cgc Arg	atc Ile	ttt Phe	aag Lys	ttt Phe 175	cgt Arg	528	
ggg Gly	gaa Glu	gga Gly	aaa Lys 180	gcg Ala	tgg Trp	gat Asp	tgg Trp	gaa Glu 185	gta Val	tca Ser	agt Ser	gaa Glu	aac Asn 190	ggc Gly	aac Asn	576	
tat Tyr	gac Asp	tat Tyr 195	tta Leu	atg Met	tat Tyr	gct Ala	gat Asp 200	gtt Val	gac Asp	tac Tyr	gac Asp	cac His 205	cct Pro	gat Asp	gtc Val	624	
gtg Val	gca Ala 210	gag Glu	aca Thr	aaa Lys	aaa Lys	tgg Trp 215	ggt Gly	atc Ile	tgg Trp	tat Tyr	gcg Ala 220	aat Asn	gaa Glu	ctg Leu	tca Ser	672	
tta Leu 225	gac Asp	ggc Gly	ttc Phe	cgt Arg	att Ile 230	gat Asp	gcc Ala	gcc Ala	aaa Lys	cat His 235	att Ile	aaa Lys	ttt Phe	tca Ser	ttt Phe 240	720	
ctg Leu	cgt Arg	gat Asp	tgg Trp	gtt Val 245	cag Gln	gcg Ala	gtc Val	aga Arg	cag Gln 250	gcg Ala	acg Thr	gga Gly	aaa Lys	gaa Glu 255	atg Met	768	
ttt Phe	acg Thr	gtt Val	gcg Ala 260	gag Glu	tat Tyr	tgg Trp	cag Gln	aat Asn 265	aat Asn	gcc Ala	ggg Gly	aaa Lys	ctc Leu 270	gaa Glu	aac Asn	816	
tac Tyr	ttg Leu	aat Asn 275	aaa Lys	aca Thr	agc Ser	ttt Phe	aat Asn 280	caa Gln	tcc Ser	gtg Val	ttt Phe	gat Asp 285	gtt Val	ccg Pro	ctt Leu	864	
cat His	ttc Phe 290	aat Asn	tta Leu	cag Gln	gcg Ala	gct Ala 295	tcc Ser	tca Ser	caa Gln	gga Gly	ggc Gly 300	gga Gly	tat Tyr	gat Asp	atg Met	912	
agg Arg 305	cgt Arg	ttg Leu	ctg Leu	gac Asp	ggt Gly 310	acc Thr	gtt Val	gtg Val	tcc Ser	agg Arg 315	cat His	ccg Pro	gaa Glu	aag Lys	gcg Ala 320	960	
gtt Val	aca Thr	ttt Phe	gtt Val	gaa Glu 325	aat Asn	cat His	gac Asp	aca Thr	cag Gln 330	ccg Pro	gga Gly	cag Gln	tca Ser	ttg Leu 335	gaa Glu	1008	
tcg Ser	aca Thr	gtc Val	caa Gln 340	act Thr	tgg Trp	ttt Phe	aaa Lys	ccg Pro 345	ctt Leu	gca Ala	tac Tyr	gcc Ala	ttt Phe 350	att Ile	ttg Leu	1056	
aca Thr	aga Arg	gaa Glu 355	tcc Ser	ggt Gly	tat Tyr	cct Pro	cag Gln 360	gtg Val	ttc Phe	tat Tyr	ggg Gly	gat Asp 365	atg Met	tac Tyr	ggg Gly	1104	
aca Thr	aaa Lys 370	ggg Gly	aca Thr	tcg Ser	cca Pro	aag Lys 375	gaa Glu	att Ile	ccc Pro	tca Ser	ctg Leu 380	aaa Lys	gat Asp	aat Asn	ata Ile	1152	
gag	ccg	att	tta	aaa	gcg	cgt	aag	gag	tac	gca	tac	ggg	ccc	cag	cac	1200	

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gat	tat	att	gac	cac	ccg	gat	gtg	atc	gga	tgg	acg	agg	gaa	ggg	gac	1248
Asp	Tyr	Ile	Asp	His 405	Pro	Asp	Val	Ile	Gly 410	Trp	Thr	Arg	Glu	Gly 415	Asp	
agc	tcc	gcc	gcc	aaa	tca	ggg	ttg	gcc	gct	tta	atc	acg	gac	gga	ccc	1296
Ser	Ser	Ala	Ala 420	Lys	Ser	Gly	Leu	Ala 425	Ala	Leu	Ile	Thr	Asp 430	Gly	Pro	
ggc	gga	tca	aag	cgg	atg	tat	gcc	ggc	ctg	aaa	aat	gcc	ggc	gag	aca	1344
Gly	Gly	Ser 435	Lys	Arg	Met	Tyr	Ala 440	Gly	Leu	Lys	Asn	Ala 445	Gly	Glu	Thr	
tgg	tat	gac	ata	acg	ggc	aac	cgt	tca	gat	act	gta	aaa	atc	gga	tct	1392
Trp	Tyr 450	Asp	Ile	Thr	Gly	Asn 455	Arg	Ser	Asp	Thr	Val 460	Lys	Ile	Gly	Ser	
gac	ggc	tgg	gga	gag	ttt	cat	gta	aac	gat	ggg	tcc	gtc	tcc	att	tat	1440
Asp 465	Gly	Trp	Gly	Glu	Phe 470	His	Val	Asn	Asp	Gly 475	Ser	Val	Ser	Ile	Tyr 480	
ggt	cag	aaa	taa													1452
Val	Gln	Lys														

<210> 14
 <211> 483
 <212> PRT
 <213> Künstliche Sequenz
 <223> Beschreibung der künstlichen Sequenz:Fusion der
 Alpha-Amylase-Gene von B. licheniformis und B.
 amyloliquefaciens (ALA34-84).

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 Gly Gln His Trp Lys Arg Leu Gln Asn Asp Ala Glu His Leu Ser Asp
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 Ile Gly Ile Thr Ala Val Trp Ile Pro Pro Ala Tyr Lys Gly Thr Ser
 35 40 45
 Gln Ala Asp Val Gly Tyr Gly Ala Tyr Asp Leu Tyr Asp Leu Gly Glu
 50 55 60
 Phe His Gln Lys Gly Thr Val Arg Thr Lys Tyr Gly Thr Lys Gly Glu
 65 70 75 80
 Leu Gln Ser Ala Ile Gly Ser Leu His Ser Arg Asn Val Gln Val Tyr
 85 90 95
 Gly Asp Val Val Leu Asn His Lys Ala Gly Ala Asp Ala Thr Glu Asp
 100 105 110
 Val Thr Ala Val Glu Val Asn Pro Ala Asn Arg Asn Gln Glu Thr Ser
 115 120 125
 Glu Glu Tyr Gln Ile Lys Ala Trp Thr Asp Phe Arg Phe Pro Gly Arg
 130 135 140
 Gly Asn Thr Tyr Ser Asp Phe Lys Trp His Trp Tyr His Phe Asp Gly
 145 150 155 160
 Ala Asp Trp Asp Glu Ser Arg Lys Ile Ser Arg Ile Phe Lys Phe Arg
 165 170 175
 Gly Glu Gly Lys Ala Trp Asp Trp Glu Val Ser Ser Glu Asn Gly Asn
 180 185 190
 Tyr Asp Tyr Leu Met Tyr Ala Asp Val Asp Tyr Asp His Pro Asp Val
 195 200 205
 Val Ala Glu Thr Lys Lys Trp Gly Ile Trp Tyr Ala Asn Glu Leu Ser

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210	Leu	Asp	Gly	Phe	Arg	Ile	Asp	Ala	Ala	Lys	His	Ile	Lys	Phe	Ser	Phe
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	Phe	Thr	Val	Ala	Glu	Tyr	Trp	Gln	Asn	Asn	Ala	Gly	Lys	Leu	Glu	Asn
	Tyr	Leu	Asn	Lys	Thr	Ser	Phe	Asn	Gln	Ser	Val	Phe	Asp	Val	Pro	Leu
	His	Phe	Asn	Leu	Gln	Ala	Ala	Ser	Ser	Gln	Gly	Gly	Gly	Tyr	Asp	Met
	Arg	Arg	Leu	Leu	Asp	Gly	Thr	Val	Val	Ser	Arg	His	Pro	Glu	Lys	Ala
305	Val	Thr	Phe	Val	Glu	Asn	His	Asp	Thr	Gln	Pro	Gly	Gln	Ser	Leu	Glu
	Ser	Thr	Val	Gln	Thr	Trp	Phe	Lys	Pro	Leu	Ala	Tyr	Ala	Phe	Ile	Leu
	Thr	Arg	Glu	Ser	Gly	Tyr	Pro	Gln	Val	Phe	Tyr	Gly	Asp	Met	Tyr	Gly
	Thr	Lys	Gly	Thr	Ser	Pro	Lys	Glu	Ile	Pro	Ser	Leu	Lys	Asp	Asn	Ile
385	Glu	Pro	Ile	Leu	Lys	Ala	Arg	Lys	Glu	Tyr	Ala	Tyr	Gly	Pro	Gln	His
	Asp	Tyr	Ile	Asp	His	Pro	Asp	Val	Ile	Gly	Trp	Thr	Arg	Glu	Gly	Asp
	Ser	Ser	Ala	Ala	Lys	Ser	Gly	Leu	Ala	Ala	Leu	Ile	Thr	Asp	Gly	Pro
	Gly	Gly	Ser	Lys	Arg	Met	Tyr	Ala	Gly	Leu	Lys	Asn	Ala	Gly	Glu	Thr
	Trp	Tyr	Asp	Ile	Thr	Gly	Asn	Arg	Ser	Asp	Thr	Val	Lys	Ile	Gly	Ser
465	Asp	Gly	Trp	Gly	Glu	Phe	His	Val	Asn	Asp	Gly	Ser	Val	Ser	Ile	Tyr
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<210> 15
 <211> 1458
 <212> DNA
 <213> Künstliche Sequenz

<220>
 <223> Beschreibung der künstlichen Sequenz:Fusion der
 Alpha-Amylase-Gene von B. licheniformis und B.
 amyloliquefaciens (LAL19-433).

<220>
 <221> CDS
 <222> (1)..(1458)

<400> 15																	
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	1				5					10					15		
	aat	gac	ggc	cag	cat	tgg	aaa	cga	ttg	cag	aat	gat	gcg	gaa	cat	tta	96
	Asn	Asp	Gly	Gln	His	Trp	Lys	Arg	Leu	Gln	Asn	Asp	Ala	Glu	His	Leu	
				20					25					30			
	tcg	gat	atc	gga	atc	act	gcc	gtc	tgg	att	cct	ccc	gca	tac	aaa	gga	144
	Ser	Asp	Ile	Gly	Ile	Thr	Ala	Val	Trp	Ile	Pro	Pro	Ala	Tyr	Lys	Gly	
			35					40					45				

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ttg	agc	caa	tcc	gat	aac	gga	tac	gga	cct	tat	gat	ttg	tat	gat	tta	192
Leu	Ser	Gln	Ser	Asp	Asn	Gly	Tyr	Gly	Pro	Tyr	Asp	Leu	Tyr	Asp	Leu	
	50					55					60					
gga	gaa	ttc	cag	caa	aaa	ggg	acg	gtc	aga	acg	aaa	tac	ggc	aca	aaa	240
Gly	Glu	Phe	Gln	Gln	Lys	Gly	Thr	Val	Arg	Thr	Lys	Tyr	Gly	Thr	Lys	
65					70					75					80	
tca	gag	ctt	caa	gat	gcg	atc	ggc	tca	ctg	cat	tcc	cgg	aac	gtc	caa	288
Ser	Glu	Leu	Gln	Asp	Ala	Ile	Gly	Ser	Leu	His	Ser	Arg	Asn	Val	Gln	
				85					90					95		
gta	tac	gga	gat	gtg	gtt	ttg	aat	cat	aag	gct	ggt	gct	gat	gca	aca	336
Val	Tyr	Gly	Asp	Val	Val	Leu	Asn	His	Lys	Ala	Gly	Ala	Asp	Ala	Thr	
			100					105					110			
gaa	gat	gta	act	gcc	gtc	gaa	gtc	aat	ccg	gcc	aat	aga	aat	cag	gaa	384
Glu	Asp	Val	Thr	Ala	Val	Glu	Val	Asn	Pro	Ala	Asn	Arg	Asn	Gln	Glu	
		115					120					125				
act	tcg	gag	gaa	tat	caa	atc	aaa	gcg	tgg	acg	gat	ttt	cgt	ttt	ccg	432
Thr	Ser	Glu	Glu	Tyr	Gln	Ile	Lys	Ala	Trp	Thr	Asp	Phe	Arg	Phe	Pro	
	130					135					140					
ggc	cgt	gga	aac	acg	tac	agt	gat	ttt	aaa	tgg	cat	tgg	tat	cat	ttc	480
Gly	Arg	Gly	Asn	Thr	Tyr	Ser	Asp	Phe	Lys	Trp	His	Trp	Tyr	His	Phe	
145					150					155					160	
gac	gga	gcg	gac	tgg	gat	gaa	tcc	cgg	aag	atc	agc	cgc	atc	ttt	aag	528
Asp	Gly	Ala	Asp	Trp	Asp	Glu	Ser	Arg	Lys	Ile	Ser	Arg	Ile	Phe	Lys	
				165					170					175		
ttt	cgt	ggg	gaa	gga	aaa	gcg	tgg	gat	tgg	gaa	gta	tca	agt	gaa	aac	576
Phe	Arg	Gly	Glu	Gly	Lys	Ala	Trp	Asp	Trp	Glu	Val	Ser	Ser	Glu	Asn	
			180					185					190			
ggc	aac	tat	gac	tat	tta	atg	tat	gct	gat	gtt	gac	tac	gac	cac	cct	624
Gly	Asn	Tyr	Asp	Tyr	Leu	Met	Tyr	Ala	Asp	Val	Asp	Tyr	Asp	His	Pro	
		195					200					205				
gat	gtc	gtg	gca	gag	aca	aaa	aaa	tgg	ggt	atc	tgg	tat	gcg	aat	gaa	672
Asp	Val	Val	Ala	Glu	Thr	Lys	Lys	Trp	Gly	Ile	Trp	Tyr	Ala	Asn	Glu	
	210					215					220					
ctg	tca	tta	gac	ggc	ttc	cgt	att	gat	gcc	gcc	aaa	cat	att	aaa	ttt	720
Leu	Ser	Leu	Asp	Gly	Phe	Arg	Ile	Asp	Ala	Ala	Lys	His	Ile	Lys	Phe	
225					230					235					240	
tca	ttt	ctg	cgt	gat	tgg	gtt	cag	gcg	gtc	aga	cag	gcg	acg	gga	aaa	768
Ser	Phe	Leu	Arg	Asp	Trp	Val	Gln	Ala	Val	Arg	Gln	Ala	Thr	Gly	Lys	
				245					250					255		
gaa	atg	ttt	acg	gtt	gcg	gag	tat	tgg	cag	aat	aat	gcc	ggg	aaa	ctc	816
Glu	Met	Phe	Thr	Val	Ala	Glu	Tyr	Trp	Gln	Asn	Asn	Ala	Gly	Lys	Leu	
			260					265					270			
gaa	aac	tac	ttg	aat	aaa	aca	agc	ttt	aat	caa	tcc	gtg	ttt	gat	gtt	864
Glu	Asn	Tyr	Leu	Asn	Lys	Thr	Ser	Phe	Asn	Gln	Ser	Val	Phe	Asp	Val	
		275					280					285				
ccg	ctt	cat	ttc	aat	tta	cag	gcg	gct	tcc	tca	caa	gga	ggc	gga	tat	912
Pro	Leu	His	Phe	Asn	Leu	Gln	Ala	Ala	Ser	Ser	Gln	Gly	Gly	Gly	Tyr	

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300

290	295																
gat atg agg cgt ttg ctg gac ggt acc gtt gtg tcc agg cat ccg gaa Asp Met Arg Arg Leu Leu Asp Gly Thr Val Val Ser Arg His Pro Glu 305 310 315 320																	960
aag gcg gtt aca ttt gtt gaa aat cat gac aca cag ccg gga cag tca Lys Ala Val Thr Phe Val Glu Asn His Asp Thr Gln Pro Gly Gln Ser 325 330 335																	1008
ttg gaa tcg aca gtc caa act tgg ttt aaa ccg ctt gca tac gcc ttt Leu Glu Ser Thr Val Gln Thr Trp Phe Lys Pro Leu Ala Tyr Ala Phe 340 345 350																	1056
att ttg aca aga gaa tcc ggt tat cct cag gtg ttc tat ggg gat atg Ile Leu Thr Arg Glu Ser Gly Tyr Pro Gln Val Phe Tyr Gly Asp Met 355 360 365																	1104
tac ggg aca aaa ggg aca tcg cca aag gaa att ccc tca ctg aaa gat Tyr Gly Thr Lys Gly Thr Ser Pro Lys Glu Ile Pro Ser Leu Lys Asp 370 375 380																	1152
aat ata gag ccg att tta aaa gcg cgt aag gag tac gca tac ggg ccc Asn Ile Glu Pro Ile Leu Lys Ala Arg Lys Glu Tyr Ala Tyr Gly Pro 385 390 400																	1200
cag cac gat tat att gac cac ccg gat gtg atc gga tgg acg agg gaa Gln His Asp Tyr Ile Asp His Pro Asp Val Ile Gly Trp Thr Arg Glu 405 410 415																	1248
ggt gac agc tcc gcc gcc aaa tca ggt ttg gcc gct tta atc acg gac Gly Asp Ser Ser Ala Ala Lys Ser Gly Leu Ala Ala Leu Ile Thr Asp 420 425 430																	1296
gga ccc ggt ggg gca aag cga atg tat gtc ggc cgg caa aac gcc ggt Gly Pro Gly Gly Ala Lys Arg Met Tyr Val Gly Arg Gln Asn Ala Gly 435 440 445																	1344
gag aca tgg cat gac att acc gga aac cgt tcg gag ccg gtt gtc atc Glu Thr Trp His Asp Ile Thr Gly Asn Arg Ser Glu Pro Val Val Ile 450 455 460																	1392
aat tcg gaa ggc tgg gga gag ttt cac gta aac ggc ggg tcg gtt tca Asn Ser Glu Gly Trp Gly Glu Phe His Val Asn Gly Gly Ser Val Ser 465 470 475 480																	1440
att tat gtt caa aga tag Ile Tyr Val Gln Arg 485																	1458

<210> 16
 <211> 485
 <212> PRT
 <213> Künstliche Sequenz
 <223> Beschreibung der künstlichen Sequenz:Fusion der
 Alpha-Amylase-Gene von B. licheniformis und B.
 amyloliquefaciens (LAL19-433).

<400> 16
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 Asn Asp Gly Gln His Trp Lys Arg Leu Gln Asn Asp Ala Glu His Leu
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      35      40      45
Leu Ser Gln Ser Asp Asn Gly Tyr Gly Pro Tyr Asp Leu Tyr Asp Leu
      50      55      60
Gly Glu Phe Gln Gln Lys Gly Thr Val Arg Thr Lys Tyr Gly Thr Lys
      65      70      75      80
Ser Glu Leu Gln Asp Ala Ile Gly Ser Leu His Ser Arg Asn Val Gln
      85      90      95
Val Tyr Gly Asp Val Val Leu Asn His Lys Ala Gly Ala Asp Ala Thr
      100      105      110
Glu Asp Val Thr Ala Val Glu Val Asn Pro Ala Asn Arg Asn Gln Glu
      115      120      125
Thr Ser Glu Glu Tyr Gln Ile Lys Ala Trp Thr Asp Phe Arg Phe Pro
      130      135      140
Gly Arg Gly Asn Thr Tyr Ser Asp Phe Lys Trp His Trp Tyr His Phe
      145      150      155      160
Asp Gly Ala Asp Trp Asp Glu Ser Arg Lys Ile Ser Arg Ile Phe Lys
      165      170      175
Phe Arg Gly Glu Gly Lys Ala Trp Asp Trp Glu Val Ser Ser Glu Asn
      180      185      190
Gly Asn Tyr Asp Tyr Leu Met Tyr Ala Asp Val Asp Tyr Asp His Pro
      195      200      205
Asp Val Val Ala Glu Thr Lys Lys Trp Gly Ile Trp Tyr Ala Asn Glu
      210      215      220
Leu Ser Leu Asp Gly Phe Arg Ile Asp Ala Ala Lys His Ile Lys Phe
      225      230      235      240
Ser Phe Leu Arg Asp Trp Val Gln Ala Val Arg Gln Ala Thr Gly Lys
      245      250      255
Glu Met Phe Thr Val Ala Glu Tyr Trp Gln Asn Asn Ala Gly Lys Leu
      260      265      270
Glu Asn Tyr Leu Asn Lys Thr Ser Phe Asn Gln Ser Val Phe Asp Val
      275      280      285
Pro Leu His Phe Asn Leu Gln Ala Ala Ser Ser Gln Gly Gly Gly Tyr
      290      295      300
Asp Met Arg Arg Leu Leu Asp Gly Thr Val Val Ser Arg His Pro Glu
      305      310      315
Lys Ala Val Thr Phe Val Glu Asn His Asp Thr Gln Pro Gly Gln Ser
      320      325      330
Leu Glu Ser Thr Val Gln Thr Trp Phe Lys Pro Leu Ala Tyr Ala Phe
      335      340      345
Ile Leu Thr Arg Glu Ser Gly Tyr Pro Gln Val Phe Tyr Gly Asp Met
      350      355      360
Tyr Gly Thr Lys Gly Thr Ser Pro Lys Glu Ile Pro Ser Leu Lys Asp
      365      370      375
Asn Ile Glu Pro Ile Leu Lys Ala Arg Lys Glu Tyr Ala Tyr Gly Pro
      380      385      390
Gln His Asp Tyr Ile Asp His Pro Asp Val Ile Gly Trp Thr Arg Glu
      395      400      405
Gly Asp Ser Ser Ala Ala Lys Ser Gly Leu Ala Ala Leu Ile Thr Asp
      410      415      420
Gly Pro Gly Gly Ala Lys Arg Met Tyr Val Gly Arg Gln Asn Ala Gly
      425      430      435
Glu Thr Trp His Asp Ile Thr Gly Asn Arg Ser Glu Pro Val Val Ile
      440      445      450
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Ile Tyr Val Gln Arg
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      485

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<211> 1452

<212> DNA

<213> Künstliche Sequenz

<220>

<223> Beschreibung der künstlichen Sequenz: Fusion der Alpha-Amylase-Gene von B. licheniformis und B. amyloliquefaciens (LAL19-153).

<220>

<221> CDS

<222> (1)..(1452)

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Asn Asp Gly Gln His Trp Lys Arg Leu Gln Asn Asp Ala Glu His Leu	
20 25 30	
tcg gat atc gga atc act gcc gtc tgg att cct ccc gca tac aaa gga	144
Ser Asp Ile Gly Ile Thr Ala Val Trp Ile Pro Pro Ala Tyr Lys Gly	
35 40 45	
ttg agc caa tcc gat aac gga tac gga cct tat gat ttg tat gat tta	192
Leu Ser Gln Ser Asp Asn Gly Tyr Gly Pro Tyr Asp Leu Tyr Asp Leu	
50 55 60	
gga gaa ttc cag caa aaa ggg acg gtc aga acg aaa tac ggc aca aaa	240
Gly Glu Phe Gln Gln Lys Gly Thr Val Arg Thr Lys Tyr Gly Thr Lys	
65 70 75 80	
tca gag ctt caa gat gcg atc ggc tca ctg cat tcc cgg aac gtc caa	288
Ser Glu Leu Gln Asp Ala Ile Gly Ser Leu His Ser Arg Asn Val Gln	
85 90 95	
gta tac gga gat gtg gtt ttg aat cat aag gct ggt gct gat gca aca	336
Val Tyr Gly Asp Val Val Leu Asn His Lys Ala Gly Ala Asp Ala Thr	
100 105 110	
gaa gat gta act gcc gtc gaa gtc aat ccg gcc aat aga aat cag gaa	384
Glu Asp Val Thr Ala Val Glu Val Asn Pro Ala Asn Arg Asn Gln Glu	
115 120 125	
act tcg gag gaa tat caa atc aaa gcg tgg acg gat ttt cgt ttt ccg	432
Thr Ser Glu Glu Tyr Gln Ile Lys Ala Trp Thr Asp Phe Arg Phe Pro	
130 135 140	
ggc cgt gga aac acg tac agt gat ttt aaa tgg cat tgg tac cat ttt	480
Gly Arg Gly Asn Thr Tyr Ser Asp Phe Lys Trp His Trp Tyr His Phe	
145 150 155 160	
gac gga acc gat tgg gac gag tcc cga aag ctg aac cgc atc tat aag	528
Asp Gly Thr Asp Trp Asp Glu Ser Arg Lys Leu Asn Arg Ile Tyr Lys	
165 170 175	
ttt caa gga aag gct tgg gat tgg gaa gtt tcc aat gaa aac ggc aac	576
Phe Gln Gly Lys Ala Trp Asp Trp Glu Val Ser Asn Glu Asn Gly Asn	
180 185 190	
tat gat tat ttg atg tat gcc gac atc gat tat gac cat cct gat gtc	624

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Tyr	Asp	Tyr	Leu	Met	Tyr	Ala	Asp	Ile	Asp	Tyr	Asp	His	Pro	Asp	Val		
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gca	gca	gaa	att	aag	aga	tgg	ggc	act	tgg	tat	gcc	aat	gaa	ctg	caa	672	
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	210					215					220						
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Leu	Asp	Gly	Phe	Arg	Leu	Asp	Ala	Val	Lys	His	Ile	Lys	Phe	Ser	Phe		
225					230					235					240		
ttg	cgg	gat	tgg	gtt	aat	cat	gtc	agg	gaa	aaa	acg	ggg	aag	gaa	atg	768	
Leu	Arg	Asp	Trp	Val	Asn	His	Val	Arg	Glu	Lys	Thr	Gly	Lys	Glu	Met		
				245					250					255			
ttt	acg	gta	gct	gaa	tat	tgg	cag	aat	gac	ttg	ggc	gcg	ctg	gaa	aac	816	
Phe	Thr	Val	Ala	Glu	Tyr	Trp	Gln	Asn	Asp	Leu	Gly	Ala	Leu	Glu	Asn		
			260					265					270				
tat	ttg	aac	aaa	aca	aat	ttt	aat	cat	tca	gtg	ttt	gac	gtg	ccg	ctt	864	
Tyr	Leu	Asn	Lys	Thr	Asn	Phe	Asn	His	Ser	Val	Phe	Asp	Val	Pro	Leu		
		275					280					285					
cat	tat	cag	ttc	cat	gct	gca	tcg	aca	cag	gga	ggc	ggc	tat	gat	atg	912	
His	Tyr	Gln	Phe	His	Ala	Ala	Ser	Thr	Gln	Gly	Gly	Gly	Tyr	Asp	Met		
	290					295					300						
agg	aaa	ttg	ctg	aac	agt	acg	gtc	gtt	tcc	aag	cat	ccg	ttg	aaa	gcg	960	
Arg	Lys	Leu	Leu	Asn	Ser	Thr	Val	Val	Ser	Lys	His	Pro	Leu	Lys	Ala		
305					310					315					320		
gtt	aca	ttt	gtc	gat	aac	cat	gat	aca	cag	ccg	ggg	caa	tcg	ctt	gag	1008	
Val	Thr	Phe	Val	Asp	Asn	His	Asp	Thr	Gln	Pro	Gly	Gln	Ser	Leu	Glu		
				325					330					335			
tcg	act	gtc	caa	aca	tgg	ttt	aag	ccg	ctt	gct	tac	gct	ttt	att	ctc	1056	
Ser	Thr	Val	Gln	Thr	Trp	Phe	Lys	Pro	Leu	Ala	Tyr	Ala	Phe	Ile	Leu		
			340					345					350				
aca	agg	gaa	tct	gga	tac	cct	cag	gtt	ttc	tac	ggg	gat	atg	tac	ggg	1104	
Thr	Arg	Glu	Ser	Gly	Tyr	Pro	Gln	Val	Phe	Tyr	Gly	Asp	Met	Tyr	Gly		
		355					360					365					
acg	aaa	gga	gac	tcc	cag	cgc	gaa	att	cct	gcc	ttg	aaa	cac	aaa	att	1152	
Thr	Lys	Gly	Asp	Ser	Gln	Arg	Glu	Ile	Pro	Ala	Leu	Lys	His	Lys	Ile		
	370					375					380						
gaa	ccg	atc	tta	aaa	gcg	aga	aaa	cag	tat	gcg	tac	gga	gca	cag	cat	1200	
Glu	Pro	Ile	Leu	Lys	Ala	Arg	Lys	Gln	Tyr	Ala	Tyr	Gly	Ala	Gln	His		
385					390					395					400		
gat	tat	ttc	gac	cac	cat	gac	att	gtc	ggc	tgg	aca	agg	gaa	ggc	gac	1248	
Asp	Tyr	Phe	Asp	His	His	Asp	Ile	Val	Gly	Trp	Thr	Arg	Glu	Gly	Asp		
				405					410					415			
agc	tcg	gtt	gca	aat	tca	ggt	ttg	gcg	gca	tta	ata	aca	gac	gga	ccc	1296	
Ser	Ser	Val	Ala	Asn	Ser	Gly	Leu	Ala	Ala	Leu	Ile	Thr	Asp	Gly	Pro		
			420					425					430				
ggt	ggg	gca	aag	cga	atg	tat	gtc	ggc	cgg	caa	aac	gcc	ggt	gag	aca	1344	
Gly	Gly	Ala	Lys	Arg	Met	Tyr	Val	Gly	Arg	Gln	Asn	Ala	Gly	Glu	Thr		
		435					440					445					

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tgg cat gac att acc gga aac cgt tcg gag ccg gtt gtc atc aat tcg 1392
 Trp His Asp Ile Thr Gly Asn Arg Ser Glu Pro Val Val Ile Asn Ser
 450 455 460

gaa ggc tgg gga gag ttt cac gta aac ggc ggg tcg gtt tca att tat 1440
 Glu Gly Trp Gly Glu Phe His Val Asn Gly Gly Ser Val Ser Ile Tyr
 465 470 475 480

ggt caa aga tag 1452
 Val Gln Arg

<210> 18

<211> 483

<212> PRT

<213> Künstliche Sequenz

<223> Beschreibung der künstlichen Sequenz:Fusion der
 Alpha-Amylase-Gene von B. licheniformis und B.
 amyloliquefaciens (LAL19-153).

<400> 18

Ala Asn Leu Asn Gly Thr Leu Met Gln Tyr Phe Glu Trp Tyr Met Pro
 1 5 10 15
 Asn Asp Gly Gln His Trp Lys Arg Leu Gln Asn Asp Ala Glu His Leu
 20 25 30
 Ser Asp Ile Gly Ile Thr Ala Val Trp Ile Pro Pro Ala Tyr Lys Gly
 35 40 45
 Leu Ser Gln Ser Asp Asn Gly Tyr Gly Pro Tyr Asp Leu Tyr Asp Leu
 50 55 60
 Gly Glu Phe Gln Gln Lys Gly Thr Val Arg Thr Lys Tyr Gly Thr Lys
 65 70 75 80
 Ser Glu Leu Gln Asp Ala Ile Gly Ser Leu His Ser Arg Asn Val Gln
 85 90 95
 Val Tyr Gly Asp Val Val Leu Asn His Lys Ala Gly Ala Asp Ala Thr
 100 105 110
 Glu Asp Val Thr Ala Val Glu Val Asn Pro Ala Asn Arg Asn Gln Glu
 115 120 125
 Thr Ser Glu Glu Tyr Gln Ile Lys Ala Trp Thr Asp Phe Arg Phe Pro
 130 135 140
 Gly Arg Gly Asn Thr Tyr Ser Asp Phe Lys Trp His Trp Tyr His Phe
 145 150 155 160
 Asp Gly Thr Asp Trp Asp Glu Ser Arg Lys Leu Asn Arg Ile Tyr Lys
 165 170 175
 Phe Gln Gly Lys Ala Trp Asp Trp Glu Val Ser Asn Glu Asn Gly Asn
 180 185 190
 Tyr Asp Tyr Leu Met Tyr Ala Asp Ile Asp Tyr Asp His Pro Asp Val
 195 200 205
 Ala Ala Glu Ile Lys Arg Trp Gly Thr Trp Tyr Ala Asn Glu Leu Gln
 210 215 220
 Leu Asp Gly Phe Arg Leu Asp Ala Val Lys His Ile Lys Phe Ser Phe
 225 230 235 240
 Leu Arg Asp Trp Val Asn His Val Arg Glu Lys Thr Gly Lys Glu Met
 245 250 255
 Phe Thr Val Ala Glu Tyr Trp Gln Asn His Ser Val Phe Asp Val Pro Leu
 260 265 270
 Tyr Leu Asn Lys Thr Asn Phe Asn His Ser Val Phe Asp Val Pro Leu
 275 280 285
 His Tyr Gln Phe His Ala Ala Ser Thr Gln Gly Gly Tyr Asp Met
 290 295 300
 Arg Lys Leu Leu Asn Ser Thr Val Val Ser Lys His Pro Leu Lys Ala
 305 310 315 320
 Val Thr Phe Val Asp Asn His Asp Thr Gln Pro Gly Gln Ser Leu Glu
 325 330 335

H04714.txt

Ser	Thr	Val	Gln	Thr	Trp	Phe	Lys	Pro	Leu	Ala	Tyr	Ala	Phe	Ile	Leu
			340					345					350		
Thr	Arg	Glu	Ser	Gly	Tyr	Pro	Gln	Val	Phe	Tyr	Gly	Asp	Met	Tyr	Gly
		355					360					365			
Thr	Lys	Gly	Asp	Ser	Gln	Arg	Glu	Ile	Pro	Ala	Leu	Lys	His	Lys	Ile
	370					375					380				
Glu	Pro	Ile	Leu	Lys	Ala	Arg	Lys	Gln	Tyr	Ala	Tyr	Gly	Ala	Gln	His
385					390					395					400
Asp	Tyr	Phe	Asp	His	His	Asp	Ile	Val	Gly	Trp	Thr	Arg	Glu	Gly	Asp
				405					410					415	
Ser	Ser	Val	Ala	Asn	Ser	Gly	Leu	Ala	Ala	Leu	Ile	Thr	Asp	Gly	Pro
			420					425					430		
Gly	Gly	Ala	Lys	Arg	Met	Tyr	Val	Gly	Arg	Gln	Asn	Ala	Gly	Glu	Thr
		435					440					445			
Trp	His	Asp	Ile	Thr	Gly	Asn	Arg	Ser	Glu	Pro	Val	Val	Ile	Asn	Ser
	450					455					460				
Glu	Gly	Trp	Gly	Glu	Phe	His	Val	Asn	Gly	Gly	Ser	Val	Ser	Ile	Tyr
465					470					475					480
Val	Gln	Arg													